```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: Wed Nov 07 10:38:58 EST 2007
============================================================



************************************************************
Reviewer Comments:
Seq Id 1 and 2

misaligned amino acid numbering.  The numbering under each 5th amino
acid is misaligned.  Do not use tab codes between numnbers use space
characters, instead.
************************************************************
```

Application No: 10573478   Version No: 1.0

Input Set:

Output Set:

Started: 2007-10-22 16:29:49.364
Finished: 2007-10-22 16:29:53.300
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 936 ms
Total Warnings: 6
Total Errors: 129
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 322	CDS location out of range SEQID (1) At Protien count (1)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (10)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (13)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (22)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (28)
E 300	Invalid codon found tta SEQID (1) POS: 46
E 323	Invalid/missing amino acid numbering SEQID (1) POS (61)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (64)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (73)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (79)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (88)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (94)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (121)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (124)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (133)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (139)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (166)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (169)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (178)

Input Set:

Output Set:

Started:	2007-10-22 16:29:49.364
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Actual SeqID Count:	22

Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (1) POS (184)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (211)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (214) This error has occured more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 322	CDS location out of range SEQID (3) At Protien count (1)
E 300	Invalid codon found ttg SEQID (3) POS: 46
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)

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gaattc atc atg cat gga gat aca cct aca ttg cat gaa tat atg tta    48
       Ile Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu
       1               5                   10

gat ttg caa cca gag aca act gat ctc tac tgt tat gag caa tta aat    96
Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn
15                  20                  25                  30

gac agc tca gag gag gag gat gaa ata gat ggt cca gct gga caa gca   144
Asp Ser Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala
                35                  40                  45

gaa ccg gac aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt   192
Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys
            50                  55                  60

gac tct acg ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt   240
Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg
        65                  70                  75

act ttg gaa gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc   288
Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile
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tgt tct cag aaa cca ggatcc          309
Cys Ser Gln Lys Pro
95
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<210> 2
<211> 99
<212> PRT
<213> Human papillomavirus type 16

<400> 2

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Ile Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu
1               5                   10                  15

Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser
            20                  25                  30

Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro
        35                  40                  45

Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser
    50                  55                  60

Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu
65                  70                  75                  80

Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser
                85                  90                  95

Gln Lys Pro
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<210> 3
<211> 330
<212> DNA
<213> Human papillomavirus type 18

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<222> (7)..(324)
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<400> 3

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gaattc agt atg cat gga cct aag gca aca ttg caa gac att gta ttg    48
       Ser Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu
        1               5                   10

cat tta gag ccc caa aat gaa att ccg gtt gac ctt cta tgt cac gag    96
His Leu Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu
15                  20                  25                  30

caa tta agc gac tca gag gaa gaa aac gat gaa ata gat gga gtt aat   144
Gln Leu Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn
                35                  40                  45
```

cat caa cat tta cca gcc cga cga gct gaa cca caa cgt cac aca atg 192
His Gln His Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met
            50   55   60

ttg tgt atg tgt tgt aag tgt gaa gcc aga att gag cta gta gta gaa 240
Leu Cys Met Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu
        65   70   75

agc tca gca gac gac ctt cga gca ttc cag cag ctg ttt ctg aac acc 288
Ser Ser Ala Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr
     80   85   90

ctg tcc ttt gtg tgt ccg tgg tgt gca tcc cag cag ggatcc   330
Leu Ser Phe Val Cys Pro Trp Cys Ala Ser Gln Gln
95   100   105

<210> 4
<211> 106
<212> PRT
<213> Human papillomavirus type 18

<400> 4

Ser Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His Leu
1   5   10   15

Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu Gln Leu
            20   25   30

Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln
        35   40   45

His Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys
     50   55   60

Met Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser
65   70   75   80

Ala Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser
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Phe Val Cys Pro Trp Cys Ala Ser Gln Gln
            100   105

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<211> 5321
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of recombinant vector pQE30-dnaK

<400> 5

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ggatcgcatc accatcacca tcacggatcc gctcgtgcgg tcgggatcga cctcgggacc 180

accaactccg tcgtctcggt tctggaaggt ggcgacccgg tcgtcgtcgc caactccgag 240

ggctccagga ccaccccgtc aattgtcgcg ttcgcccgca acggtgaggt gctggtcggc 300

cagcccgcca agaaccaggc agtgaccaac gtcgatcgca ccgtgcgctc ggtcaagcga 360

cacatgggca gcgactggtc catagagatt gacggcaaga aatacaccgc gccggagatc 420

agcgcccgca ttctgatgaa gctgaagcgc gacgccgagg cctacctcgg tgaggacatt 480

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atccaggtct atcaggggga gcgtgagatc gccgcgcaca acaagttgct cgggtccttc 1440

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<213> Bos taurus

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<210> 8
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Ser

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ctgaaagctt   130

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<223> Reverse primer for pHE718

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10